



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/083,842
Source: OIPE
Date Processed by STIC: 3/19/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

OPE

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/083,842</u>
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ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

**Does Not Comply
Corrected Diskette Needed**

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/083,842

DATE: 03/19/2002
TIME: 16:15:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\03192002\J083842.raw

→ The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

3 <110> APPLICANT: Syngenta Biotechnology, Inc.
4 Grina, Jonas
6 <120> TITLE OF INVENTION: NOVEL CYANOENAMINES USEFUL AS LIGANDS FOR MODULATING GENE
EXPRESSION IN
7 PLANTS OR ANIMALS
9 <130> FILE REFERENCE: 1392/2/2
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/083,842
C--> 11 <141> CURRENT FILING DATE: 2002-02-27
11 <150> PRIOR APPLICATION NUMBER: 60/272,905
12 <151> PRIOR FILING DATE: 2001-03-02
14 <160> NUMBER OF SEQ ID NOS: 12
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 17
20 <212> TYPE: DNA
21 <213> ORGANISM: synthetic construct
23 <400> SEQUENCE: 1
24 agcttgaggg tataatg 17
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 17
29 <212> TYPE: DNA
30 <213> ORGANISM: synthetic construct
32 <400> SEQUENCE: 2
33 actcccatat tactcga 17
36 <210> SEQ ID NO: 3
37 <211> LENGTH: 36
38 <212> TYPE: DNA
39 <213> ORGANISM: synthetic construct
41 <400> SEQUENCE: 3
42 gatccgagac aagggttcaa tgcacttgtc caatga 36
45 <210> SEQ ID NO: 4
46 <211> LENGTH: 36
47 <212> TYPE: DNA
48 <213> ORGANISM: synthetic construct
50 <400> SEQUENCE: 4
51 gctctgttcc caagttagt gaacaggta ctctag 36
54 <210> SEQ ID NO: 5
55 <211> LENGTH: 147
56 <212> TYPE: DNA
57 <213> ORGANISM: synthetic construct
59 <400> SEQUENCE: 5
60 gatccgagac aagggttcaa tgcacttgtc caatgagatc cgagacaagg gttcaatgca 60
62 cttgtccat gagatctcat tggacaagtg cattgaacct tgtctcgat ctcattggac 120
64 aagtgcattg aacccttgc tcggat 147

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Input Set : A:\EP.txt
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67 <210> SEQ ID NO: 6
68 <211> LENGTH: 2840
69 <212> TYPE: DNA
70 <213> ORGANISM: Manduca sexta
72 <220> FEATURE:
73 <221> NAME/KEY: CDS
74 <222> LOCATION: (361)..(2031)
75 <223> OTHER INFORMATION:
78 <400> SEQUENCE: 6
79 tccgttgcac acggtcgac gctgtcaacg tgctcgaaaa tacggctcaa gcgaacgcgt 60
81 aaccccgctc tccacatcac cgagcgaact ctagaactcg cgtactttc tcacctgttg 120
83 cttcgattg tgggtgact gaaaagcgcac gctgtatcgat gtcgaagatt ctctataagt 180
85 gcataatata ttccgagacag tggatagcga ttccgttccgg tttcatcgcc cggatgatgtg 240
87 gttcatgccc gtagagacgc gtttagatacg ttatggcgag gaaaaagtga agtggaaagcc 300
89 tacgtcagag gatgtccctc ggtggtcacg gaagccgggg cgtgtgacgc gctcttcgac 360
91 atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt 408
92 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
93 1 5 10 15
95 gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg 456
96 Glu Glu Ser Ser Glu Val Thr Ser Ser Ala Phe Gly Met Pro
97 20 25 30
99 gcg gcc atg gta atg tca ccg gag tcg ctg gcg tcg cca gag tac ggc 504
100 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
101 35 40 45
103 ggc ctc gag ctc tgg agc tac gat gag acc atg aca aac tat ccg gcg 552
104 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
105 50 55 60
107 cag tca ctg ctc ggc gcg tgt aat gcg ccg cag cag cag caa cag 600
108 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln
109 65 70 75 80
111 caa caa cag cag ccg tcc gct cag ccg ctg ccg tct atg ccg ctg ccg 648
112 Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
113 85 90 95
115 atg cct cct aca act cct aaa tca gag aac gag tcc atg tcg tca ggt 696
116 Met Pro Pro Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
117 100 105 110
119 cga gaa gaa tta tca ccg gcc tca agt ata aat gga tgt agt act gat 744
120 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
121 115 120 125
123 ggg gaa cca aga cga cag aag aaa ggg cca gcg ccg cgc cag cag gag 792
124 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
125 130 135 140
127 gaa ctg tgc ctt gtt tgc ggc gac agg gct tcg gga tat cac tat aac 840
128 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
129 145 150 155 160
131 gcg ctt acg tgc gaa gga tgt aaa ggg ttc ttc agg cgg agt gtg acc 888
132 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
133 165 170 175
135 aag aat gcg gta tat att tgt aaa ttt gga cac gcc tgc gag atg gac 936

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136	Lys	Asn	Ala	Val	Tyr	Ile	Cys	Lys	Phe	Gly	His	Ala	Cys	Glu	Met	Asp		
137			180				185							190				
139	atg	tac	atg	agg	aga	aaa	tgc	caa	gag	tgt	cgg	ttg	aag	aaa	tgc	ctc	984	
140	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu		
141			195				200							205				
143	gcg	gtg	ggc	atg	agg	ccc	gag	tgc	gtc	gtc	cca	gag	tcc	acg	tgc	aag	1032	
144	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Ser	Thr	Cys	Lys		
145			210				215							220				
147	aac	aaa	aga	aga	gaa	aag	gaa	gca	cag	aga	gaa	aaa	gac	aaa	ctg	cca	1080	
148	Asn	Lys	Arg	Arg	Glu	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Leu	Pro		
149	225			230			235							240				
151	gtc	agt	acg	acg	aca	gtg	gac	gat	cat	atg	cct	gcc	ata	atg	caa	tgt	1128	
152	Val	Ser	Thr	Thr	Val	Asp	Asp	His	Met	Pro	Ala	Ile	Met	Gln	Cys			
153			245				250							255				
155	gac	cct	ccg	ccc	cca	gag	gcg	gca	agg	att	cac	gaa	gtg	gtc	ccg	agg	1176	
156	Asp	Pro	Pro	Pro	Glu	Ala	Ala	Arg	Ile	His	Glu	Val	Val	Pro	Arg			
157			260				265							270				
159	ttc	cta	acg	gag	aag	cta	atg	gag	cag	aac	aga	ctg	aag	aat	gtg	acg	1224	
160	Phe	Leu	Thr	Glu	Lys	Leu	Met	Glu	Gln	Asn	Arg	Leu	Lys	Asn	Val	Thr		
161			275				280							285				
163	ccg	ctg	tcg	gcg	aac	cag	aag	tcc	ctg	atc	gct	agg	ctc	gtg	tgg	tac	1272	
164	Pro	Leu	Ser	Ala	Asn	Gln	Lys	Ser	Leu	Ile	Ala	Arg	Leu	Val	Trp	Tyr		
165			290				295							300				
167	cag	gag	ggg	tac	gag	cag	ccg	tcg	gag	gaa	gat	ctc	aag	aga	gtt	aca	1320	
168	Gln	Glu	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	Leu	Lys	Arg	Val	Thr		
169	305			310			315							320				
171	cag	aca	tgg	cag	tta	gaa	gaa	gaa	gag	gag	gaa	act	gac	atg	ccc		1368	
172	Gln	Thr	Trp	Gln	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Asp	Met	Pro			
173			325				330							335				
175	ttc	cgt	cag	ata	gac	atg	acg	atc	tta	aca	gtg	cag	ctt	att	gtt		1416	
176	Phe	Arg	Gln	Ile	Thr	Glu	Met	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile	Val		
177			340				345							350				
179	gaa	ttc	gca	aag	gga	cta	ccg	gga	ttc	tcc	aag	ata	tct	cag	tcc	gat		
180	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Gly	Phe	Ser	Lys	Ile	Ser	Gln	Ser	Asp		
181			355				360							365				
183	caa	att	aca	tta	tta	aag	gcg	tca	tca	agc	gaa	gtg	atg	atg	ctg	cga	1512	
184	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Ser	Ser	Ser	Ser	Glu	Val	Met	Met	Leu	Arg	
185			370				375							380				
187	gtg	gcg	cga	cg	tac	gac	g	cg	g	cg	ac	g	gt	at	ct		1560	
188	Val	Ala	Arg	Arg	Tyr	Asp	Ala	Ala	Thr	Asp	Ser	Val	Leu	Phe	Ala	Asn		
189	385			390			395							400				
191	aac	cag	cg	tac	ac	cg	g	ac	tac	cg	aag	g	cg	at	tcc	tac	1608	
192	Asn	Gln	Ala	Tyr	Thr	Arg	Asp	Asn	Tyr	Arg	Lys	Ala	Gly	Met	Ser	Tyr		
193			405				410							415				
195	gtc	atc	gag	gac	ctg	ctg	cac	ttc	tgt	cg	tgt	at	tg	tcc	at	tg		
196	Val	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Cys	Met	Tyr	Ser	Met	Ser		
197			420				425							430				
199	atg	gac	aat	gtg	cac	tac	g	cg	ctg	ctc	acc	gcc	at	gt	at	tcc	tc	1704
200	Met	Asp	Asn	Val	His	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	Phe	Ser		

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283 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln
284 65 70 75 80
287 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
288 85 90 95
291 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
292 100 105 110
295 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
296 115 120 125
299 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
300 130 135 140
303 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
304 145 150 155 160
307 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
308 165 170 175
311 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
312 180 185 190
315 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
316 195 200 205
319 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys
320 210 215 220
323 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
324 225 230 235 240
327 Val Ser Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
328 245 250 255
331 Asp Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
332 260 265 270
335 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
336 275 280 285
339 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
340 290 295 300
343 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
344 305 310 315 320
347 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
348 325 330 335
351 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
352 340 345 350
355 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
356 355 360 365
359 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
360 370 375 380
363 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
364 385 390 395 400
367 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
368 405 410 415
371 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
372 420 425 430
375 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
376 435 440 445
379 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg

VERIFICATION SUMMARY
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Input Set : A:\EP.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date